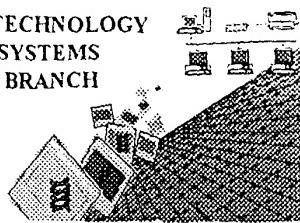


BIOTECHNOLOGY
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RAW SEQUENCE LISTING
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PATENT APPLICATION: US/09/989,025

DATE: 02/19/2002
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Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\02192002\I989025.raw

P4 TECH CENTER 1600/2900

3 <110> APPLICANT: NAKAI, JUNICHI
5 <120> TITLE OF INVENTION: METHOD FOR PRODUCING A BIOSENSOR PROTEIN CAPABLE OF
REGULATING A

6 FLUORECENCE PROPERTY OF GREEN FLUORECENT PROTEIN, AND THE BIOSENSOR PROTEIN
7 PRODUCED BY THE METHOD

9 <130> FILE REFERENCE: 216339US0

11 <140> CURRENT APPLICATION NUMBER: 09/989,025

12 <141> CURRENT FILING DATE: 2001-11-21

14 <150> PRIOR APPLICATION NUMBER: JP/2000-356047

15 <151> PRIOR FILING DATE: 2000-11-22

17 <160> NUMBER OF SEQ ID NOS: 17

19 <170> SOFTWARE: PatentIn version 3.1

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 717

23 <212> TYPE: DNA

24 <213> ORGANISM: Aequorea victoria

26 <220> FEATURE:

27 <221> NAME/KEY: CDS

28 <222> LOCATION: (1)..(717)

29 <223> OTHER INFORMATION:

32 <400> SEQUENCE: 1

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34 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val

35 1 5 10 15

37 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96

38 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu

39 20 25 30

41 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144

42 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

43 35 40 45

45 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg

46 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu

47 50 55 60

49 acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag 240

50 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln

51 65 70 75 80

53 cac gac ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288

54 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

55 85 90 95

57 acc atc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336

58 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

59 100 105 110

61 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384

62 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

Does Not Comply
Corrected Diskette Needed

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PATENT APPLICATION: US/09/989,025

DATE: 02/19/2002
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Input Set : A:\PTO.VSK.txt
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63	115	120	125	
65	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac			432
66	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
67	130	135	140	
69	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aac gac ggc			480
70	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly			
71	145	150	155	160
73	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg			528
74	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val			
75	165	170	175	
77	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc			576
78	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro			
79	180	185	190	
81	gtg ctg ctc gac aac cac tac ctg agc acc cag tcc gcc ctg agc			624
82	Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser			
83	195	200	205	
85	aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg			672
86	Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val			
87	210	215	220	
89	acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa			717
90	Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys			
91	225	230	235	
94	<210> SEQ ID NO: 2			
95	<211> LENGTH: 238			
96	<212> TYPE: PRT			
97	<213> ORGANISM: Aequorea victoria			
99	<400> SEQUENCE: 2			
101	Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val			
102	1	5	10	15
105	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu			
106	20	25	30	
109	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
110	35	40	45	
113	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu			
114	50	55	60	
117	Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln			
118	65	70	75	80
121	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
122	85	90	95	
125	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
126	100	105	110	
129	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile			
130	115	120	125	
133	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
134	130	135	140	
137	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly			
138	145	150	155	160
141	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val			
142	165	170	175	

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PATENT APPLICATION: US/09/989,025

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Input Set : A:\PTO.VSK.txt
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145 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
146 180 185 190
149 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
150 195 200 205
153 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
154 210 215 220
157 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
158 225 230 235
161 <210> SEQ ID NO: 3
162 <211> LENGTH: 447
163 <212> TYPE: DNA
164 <213> ORGANISM: Rattus norvegicus
166 <220> FEATURE:
167 <221> NAME/KEY: CDS
168 <222> LOCATION: (1)..(444)
169 <223> OTHER INFORMATION:
172 <400> SEQUENCE: 3
173 gct gac caa ctg act gaa gag cag atc gca gaa ttc aaa gaa gct ttc 48
174 Ala Asp Gln Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe
175 1 5 10 15
177 tcc cta ttt gac aag gac ggg gat ggg aca ata aca acc aag gag ctg 96
178 Ser Leu Phe Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu
179 20 25 30
181 ggg acg gtg atg cgg tct ctg ggg cag aac ccc aca gaa gca gag ctg 144
182 Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu
183 35 40 45
185 cag gac atg atc aat gaa gta gat gcc gac ggt aat ggc aca atc gac 192
186 Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp
187 50 55 60
189 ttc cct gaa ttc ctg aca atg atg gca aga aaa atg aaa gac aca gac 240
190 Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Asp
191 65 70 75 80
193 agt gaa gaa att aga gaa gcg ttc cgt gtg ttt gat aag gat ggc 288
194 Ser Glu Glu Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp Gly
195 85 90 95
197 aat ggc tac atc agt gca gca gag ctt cgc cac gtg atg aca aac ctt 336
198 Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu
199 100 105 110
201 gga gag aag tta aca gat gaa gag gtt gat gaa atg atc agg gaa gca 384
202 Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala
203 115 120 125
205 gac atc gat ggg gat ggt cag gta aac tac gaa gag ttt gta caa atg 432
206 Asp Ile Asp Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met
207 130 135 140
209 atg aca gcg aag tga 447
210 Met Thr Ala Lys
211 145
214 <210> SEQ ID NO: 4
215 <211> LENGTH: 148

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Input Set : A:\PTO.VSK.txt
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216 <212> TYPE: PRT
 217 <213> ORGANISM: Rattus norvegicus
 219 <400> SEQUENCE: 4
 221 Ala Asp Gln Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe
 222 1 5 10 15
 225 Ser Leu Phe Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu
 226 20 25 30
 229 Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu
 230 35 40 45
 233 Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp
 234 50 55 60
 237 Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Asp
 238 65 70 75 80
 241 Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp Gly
 242 85 90 95
 245 Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu
 246 100 105 110
 249 Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala
 250 115 120 125
 253 Asp Ile Asp Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met
 254 130 135 140
 257 Met Thr Ala Lys
 258 145
 261 <210> SEQ ID NO: 5
 262 <211> LENGTH: 63
 263 <212> TYPE: DNA
 264 <213> ORGANISM: Artificial Sequence
 266 <220> FEATURE:
 267 <223> OTHER INFORMATION: Synthetic DNA
 269 <220> FEATURE:
 270 <221> NAME/KEY: CDS
 271 <222> LOCATION: (1)..(63)
 272 <223> OTHER INFORMATION:
 275 <400> SEQUENCE: 5
 276 tca tca cgt cgt aag tgg aat aag aca ggt cac gca gtc aga gct ata 48
 277 Ser Ser Arg Arg Lys Trp Asn Lys Thr Gly His Ala Val Arg Ala Ile
 278 1 5 10 15
 280 ggt cgg ctg agc tca 63
 281 Gly Arg Leu Ser Ser
 282 20
 285 <210> SEQ ID NO: 6
 286 <211> LENGTH: 21
 287 <212> TYPE: PRT
 288 <213> ORGANISM: Artificial Sequence
 290 <220> FEATURE:
 291 <223> OTHER INFORMATION: Synthetic DNA This is an amino acid sequence, a peptide
 293 <400> SEQUENCE: 6
 295 Ser Ser Arg Arg Lys Trp Asn Lys Thr Gly His Ala Val Arg Ala Ile
 296 1 5 10 15

Please correct any subsequent
sequence showing the above error.

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Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\02192002\I989025.raw

299 Gly Arg Leu Ser Ser
 300 20
 303 <210> SEQ ID NO: 7
 304 <211> LENGTH: 1251
 305 <212> TYPE: DNA
 306 <213> ORGANISM: Artificial Sequence
 308 <220> FEATURE:
 309 <223> OTHER INFORMATION: Synthetic DNA
 311 <220> FEATURE:
 312 <221> NAME/KEY: CDS
 313 <222> LOCATION: (1)..(1248)
 314 <223> OTHER INFORMATION:
 317 <400> SEQUENCE: 7
 318 atg gtc gac tca tca cgt cgt aag tgg aat aag aca ggt cac gca gtc 48
 319 Met Val Asp Ser Ser Arg Arg Lys Trp Asn Lys Thr Gly His Ala Val
 320 1 5 10 15
 322 aga gct ata ggt cgg ctg agc tca ctc gag aac gtc tat atc atg gcc 96
 323 Arg Ala Ile Gly Arg Leu Ser Ser Leu Glu Asn Val Tyr Ile Met Ala
 324 20 25 30
 326 gac aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac 144
 327 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
 328 35 40 45
 330 atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc 192
 331 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
 332 50 55 60
 334 ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc 240
 335 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
 336 65 70 75 80
 338 acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg 288
 339 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
 340 85 90 95
 342 gtc ctg ctg gag ttc gtg acc gcc ggg atc act ctc ggc atg gac 336
 343 Val Leu Leu Glu Phe Val Thr Ala Gly Ile Thr Leu Gly Met Asp
 344 100 105 110
 346 gag ctg tac aag ggc ggt acc gga ggg agc atg gtg agc aag ggc gag 384
 347 Glu Leu Tyr Lys Gly Gly Thr Gly Ser Met Val Ser Lys Gly Glu
 348 115 120 125
 350 gag ctg ttc acc ggg gtg ccc atc ctg gtc gag ctg gac ggc gac 432
 351 Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
 352 130 135 140
 354 gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gac ggc gat gcc 480
 355 Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
 356 145 150 155 160
 358 acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg 528
 359 Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
 360 165 170 175
 362 ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tac ggc gtg cag 576
 363 Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln
 364 180 185 190

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/989,025

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